

**Table 4: Human 5T4 9mers binding to HLA A 0201**

*B concd.*

Rank	Start	Sequence	Dissociation Time
1	97	FLTGNQLAV (SEQ ID NO:5)	319.939
2	364	ALIGAIFLL (SEQ ID NO:6)	284.974
3	351	SLQTSYVFL (SEQ ID NO:7)	176.240
4	368	AIFLLVLYL (SEQ ID NO:8)	137.482
5	283	GLPHIRVFL (SEQ ID NO:9)	117.493
6	358	FLGIVLALI (SEQ ID NO:10)	110.379
7	81	NLTEVPTDL (SEQ ID NO:11)	87.586
8	95	NLFLTGNQL (SEQ ID NO:12)	79.041
9	222	FLYLPRDVL (SEQ ID NO:13)	63.174
10	373	VLYLNRKGI (SEQ ID NO:14)	56.754
11	365	LIGAIFLLV (SEQ ID NO:15)	30.890
12	290	FLDNNPWVC (SEQ ID NO:16)	28.109
13	301	HMADMVTWL (SEQ ID NO:17)	27.207

**Table 5: Murine 5T4 9mers binding to human HLA A 0201**

Rank	Start	Sequence	Dissociation Time
1	307	YMADMVAWL (SEQ ID NO:18)	3680.892
2	81	NLLEVPAVL (SEQ ID NO:19)	324.068
3	97	FLTGNQMTV (SEQ ID NO:20)	319.939
4	370	ALIGAIFLL (SEQ ID NO:21)	284.974
5	228	FLFLPRDLL (SEQ ID NO:22)	178.158
6	357	SLQTSYVFL (SEQ ID NO:23)	176.240
7	374	AIFLLVLYL (SEQ ID NO:24)	137.482
8	289	GLAHVKVFL (SEQ ID NO:25)	117.493
9	364	FLGIVLALI (SEQ ID NO:26)	110.379
10	379	VLYLNRKG (SEQ ID NO:27)	56.754

Kindly replace the sentence found on page 55, line 11, with the following new sentence:

The above data derived from the Parker Peptide Binding Predictions Programme indicates that mutation of the human AA sequence starting at position 301 from YMADMVAWL (SEQ ID NO:18) when changed to HMADMVTWL (SEQ ID NO:17) leads to a 10 fold increase in half time of dissociation to HLA A0201.